

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: VAN ALSTYNE, Diane
SHARMA, Lawrence Rajendra
- (ii) TITLE OF INVENTION: PEPTIDES REPRESENTING EPITOPIC SITES FOR
BACTERIAL AND VIRAL MENINGITIS CAUSING AGENTS AND THEIR CNS
CARRIER, ANTIBODIES THERETO, AND USES THEREOF
- (iii) NUMBER OF SEQUENCES: 75
- (iv) CORRESPONDENCE ADDRESS:
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 - (C) CITY: San Diego Washington
 - (D) STATE: California ~~D.C.~~
 - (E) COUNTRY: USA
 - (F) ZIP: 92037 ~~20007-5109~~
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/489,850 ~~08/486,050~~
 - (B) FILING DATE: 24-JAN-2000 ~~07-JUN-1995~~
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/486,050
 - (B) FILING DATE: 07-JUN-1995
 - (C) APPLICATION NUMBER: US 08/127,499
 - (D) FILING DATE: 28-SEP-1993
- (viii) ATTORNEY/AGENT INFORMATION:
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~~BENT, Stephen A.~~
 - (B) REGISTRATION NUMBER: 50,448 ~~29,768~~
 - (C) REFERENCE/DOCKET NUMBER: VANALYSTYNE-P001
~~51916/103/INBI~~
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 992 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ala	Ser	Thr	Thr	Pro	Ile	Thr	Met	Glu	Asp	Leu	Gln	Lys	Ala	Leu
1				5					10					15	
Glu	Ala	Gln	Ser	Arg	Ala	Leu	Arg	Ala	Gly	Leu	Ala	Ala	Gly	Ala	Ser
			20					25					30		

79

His	Met	Asp	Phe	Trp	Cys	Val	Glu	His	Asp	Arg	Pro	Pro	Pro	Ala	Thr	385	390	395	400
Pro	Thr	Ser	Leu	Thr	Thr	Ala	Ala	Asn	Tyr	Ile	Ala	Ala	Ala	Thr	Pro	405	410	415	
Ala	Thr	Ala	Pro	Pro	Pro	Cys	His	Ala	Gly	Leu	Asn	Asp	Ser	Cys	Gly	420	425	430	
Gly	Phe	Leu	Ser	Gly	Cys	Gly	Pro	Met	Arg	Leu	Pro	Thr	Ala	Leu	Thr	435	440	445	
Pro	Gly	Ala	Val	Gly	Asp	Leu	Arg	Ala	Val	His	His	Arg	Pro	Val	Pro	450	455	460	
Ala	Tyr	Pro	Val	Cys	Cys	Ala	Met	Arg	Trp	Gly	Leu	Pro	Pro	Trp	Glu	465	470	475	480
Leu	Val	Ile	Leu	Thr	Ala	Arg	Pro	Glu	Asp	Gly	Trp	Thr	Cys	Arg	Gly	485	490	495	
Val	Pro	Ala	His	Pro	Gly	Thr	Arg	Cys	Pro	Glu	Leu	Val	Ser	Pro	Met	500	505	510	
Gly	Arg	Ala	Thr	Cys	Ser	Pro	Ala	Ser	Ala	Leu	Trp	Leu	Ala	Thr	Ala	515	520	525	
Asn	Ala	Leu	Ser	Leu	Asp	His	Ala	Phe	Ala	Ala	Phe	Val	Leu	Leu	Val	530	535	540	
Pro	Trp	Val	Leu	Ile	Phe	Met	Val	Cys	Arg	Arg	Ala	Cys	Arg	Arg	Pro	545	550	555	560
Ala	Pro	Pro	Pro	Pro	Ser	Pro	Gln	Ser	Ser	Cys	Arg	Gly	Thr	Thr	Pro	565	570	575	
Pro	Ala	Tyr	Gly	Glu	Glu	Ala	Phe	Thr	Tyr	Leu	Cys	Thr	Ala	Pro	Gly	580	585	590	
Cys	Ala	Thr	Gln	Thr	Pro	Val	Pro	Val	Arg	Leu	Ala	Gly	Val	Gly	Phe	595	600	605	
Glu	Ser	Lys	Ile	Val	Asp	Gly	Gly	Cys	Phe	Ala	Pro	Trp	Asp	Leu	Glu	610	615	620	
Ala	Thr	Gly	Ala	Cys	Ile	Cys	Glu	Ile	Pro	Thr	Asp	Val	Ser	Cys	Glu	625	630	635	640
Gly	Leu	Gly	Ala	Trp	Val	Pro	Thr	Ala	Pro	Cys	Ala	Arg	Ile	Trp	Asn	645	650	655	
Gly	Thr	Gln	Arg	Ala	Cys	Thr	Phe	Trp	Ala	Val	Asn	Ala	Tyr	Ser	Ser	660	665	670	
Gly	Gly	Tyr	Ala	Gln	Leu	Ala	Ser	Tyr	Phe	Asn	Pro	Gly	Gly	Ser	Tyr	675	680	685	
Tyr	Lys	Gln	Tyr	His	Pro	Thr	Ala	Cys	Glu	Val	Glu	Pro	Ala	Phe	Gly	690	695	700	
His	Ser	Asp	Ala	Ala	Cys	Trp	Gly	Phe	Pro	Thr	Asp	Thr	Val	Met	Ser	705	710	715	720
Val	Phe	Ala	Leu	Ala	Ser	Tyr	Val	Gln	His	Pro	His	Lys	Thr	Val	Arg	725	730	735	

Val	Lys	Phe	His	Thr	Glu	Thr	Arg	Thr	Val	Trp	Gln	Leu	Ser	Val	Ala	
			740					745					750			
Gly	Val	Ser	Cys	Asn	Val	Thr	Thr	Glu	His	Pro	Phe	Cys	Asn	Thr	Pro	
		755					760					765				
His	Gly	Gln	Leu	Glu	Val	Gln	Val	Pro	Pro	Asp	Pro	Gly	Asp	Leu	Val	
	770					775					780					
Glu	Tyr	Ile	Met	Asn	Tyr	Thr	Gly	Asn	Gln	Gln	Ser	Arg	Trp	Gly	Leu	
785					790					795					800	
Gly	Ser	Pro	Asn	Cys	His	Gly	Pro	Asp	Trp	Ala	Ser	Pro	Val	Cys	Gln	
			805						810					815		
Arg	His	Ser	Pro	Asp	Cys	Ser	Arg	Leu	Val	Gly	Ala	Thr	Pro	Glu	Arg	
			820					825					830			
Pro	Arg	Leu	Arg	Leu	Val	Asp	Ala	Asp	Asp	Pro	Leu	Leu	Arg	Thr	Ala	
		835					840					845				
Pro	Gly	Pro	Gly	Glu	Val	Trp	Val	Thr	Pro	Val	Ile	Gly	Ser	Gln	Ala	
	850					855					860					
Arg	Lys	Cys	Gly	Leu	His	Ile	Arg	Ala	Gly	Pro	Tyr	Gly	His	Ala	Thr	
865					870					875					880	
Val	Glu	Met	Pro	Glu	Trp	Ile	His	Ala	His	Thr	Thr	Ser	Asp	Pro	Trp	
				885					890					895		
His	Pro	Pro	Gly	Pro	Leu	Gly	Leu	Lys	Phe	Lys	Thr	Val	Arg	Pro	Val	
			900					905					910			
Ala	Leu	Pro	Arg	Ala	Leu	Ala	Pro	Pro	Arg	Asn	Val	Arg	Val	Thr	Gly	
		915					920					925				
Cys	Tyr	Gln	Cys	Gly	Thr	Pro	Ala	Leu	Val	Glu	Gly	Leu	Ala	Pro	Gly	
	930					935					940					
Gly	Gly	Asn	Cys	His	Leu	Thr	Val	Asn	Gly	Glu	Asp	Val	Gly	Ala	Phe	
945					950					955					960	
Pro	Pro	Gly	Lys	Phe	Val	Thr	Ala	Ala	Leu	Leu	Asn	Thr	Pro	Pro	Pro	
				965					970					975		
Tyr	Gln	Val	Ser	Cys	Gly	Gly	Glu	Ser	Asp	Arg	Ala	Ser	Ala	Gly	His	
			980					985					990			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Pro	Ser	Arg	Ala	Pro	Pro	Gln	Gln	Pro	Gln	Pro	Pro	Arg	Met	Gln	Thr
1				5				10						15	

Gly Arg Gly Gly Ser
20

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln Pro Gln Pro Pro Arg Met
1 5

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro Ser Arg
1 5 10 15
Ala Pro Pro Gln Gln
20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gln Thr Pro Ala Pro Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Asp Met Ala Ala Pro Pro Met Pro Pro Gln Pro Pro Arg Ala His Gly
1 5 10 15
Gln His Tyr Gly His
20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Pro Pro Gln Pro Pro Arg Ala
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1063 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ala Ser Thr Thr Pro Ile Thr Met Glu Asp Leu Gln Lys Ala Leu
1 5 10 15
Glu Ala Gln Ser Arg Ala Leu Arg Ala Glu Leu Ala Ala Gly Ala Ser
20 25 30
Gln Ser Arg Arg Pro Arg Pro Pro Arg Gln Arg Asp Ser Ser Thr Ser
35 40 45
Gly Asp Asp Ser Gly Arg Asp Ser Gly Gly Pro Arg Arg Arg Gly
50 55 60
Asn Arg Gly Arg Gly Gln Arg Arg Asp Trp Ser Arg Ala Pro Pro Pro
65 70 75 80
Pro Glu Glu Arg Gln Glu Ser Arg Ser Gln Thr Pro Ala Pro Lys Pro
85 90 95
Ser Arg Ala Pro Pro Gln Gln Pro Gln Pro Pro Arg Met Gln Thr Gly
100 105 110
Arg Gly Gly Ser Ala Pro Arg Pro Glu Leu Gly Pro Pro Thr Asn Pro
115 120 125
Phe Gln Ala Ala Val Ala Arg Gly Leu Arg Pro Pro Leu His Asp Pro
130 135 140

Asp	Thr	Glu	Ala	Pro	Thr	Glu	Ala	Cys	Val	Thr	Ser	Trp	Leu	Trp	Ser		
145					150					155					160		
Glu	Gly	Gln	Gly	Ala	Val	Phe	Tyr	Arg	Val	Asp	Leu	His	Phe	Thr	Asn		
				165					170					175			
Leu	Gly	Thr	Pro	Pro	Leu	Asp	Glu	Asp	Gly	Arg	Trp	Asp	Pro	Ala	Leu		
			180					185					190				
Met	Tyr	Asn	Pro	Cys	Gly	Pro	Glu	Pro	Pro	Ala	His	Val	Val	Arg	Ala		
		195					200					205					
Tyr	Asn	Gln	Pro	Ala	Gly	Asp	Val	Arg	Gly	Val	Trp	Gly	Lys	Gly	Glu		
	210					215					220						
Arg	Thr	Tyr	Ala	Glu	Gln	Asp	Phe	Arg	Val	Gly	Gly	Thr	Arg	Trp	His		
225					230					235					240		
Arg	Leu	Leu	Arg	Met	Pro	Val	Arg	Gly	Leu	Asp	Gly	Asp	Ser	Ala	Pro		
				245					250					255			
Leu	Pro	Pro	His	Thr	Thr	Glu	Arg	Ile	Glu	Thr	Arg	Ser	Ala	Arg	His		
			260					265					270				
Pro	Trp	Arg	Ile	Arg	Phe	Gly	Ala	Pro	Gln	Ala	Phe	Leu	Ala	Gly	Leu		
		275					280					285					
Leu	Leu	Ala	Thr	Val	Ala	Val	Gly	Thr	Ala	Arg	Ala	Gly	Leu	Gln	Pro		
	290					295					300						
Arg	Ala	Asp	Met	Ala	Ala	Pro	Pro	Thr	Leu	Pro	Gln	Pro	Pro	Cys	Ala		
305					310					315					320		
His	Gly	Gln	His	Tyr	Gly	His	His	His	His	Gln	Leu	Pro	Phe	Leu	Gly		
			325						330					335			
His	Asp	Gly	His	His	Gly	Gly	Thr	Leu	Arg	Val	Gly	Gln	His	Tyr	Arg		
			340					345					350				
Asn	Ala	Ser	Asp	Val	Leu	Pro	Gly	His	Trp	Leu	Gln	Gly	Gly	Trp	Gly		
		355					360					365					
Cys	Tyr	Asn	Leu	Ser	Asp	Trp	His	Gln	Gly	Thr	His	Val	Cys	His	Thr		
	370					375					380						
Lys	His	Met	Asp	Phe	Trp	Cys	Val	Glu	His	Ala	Arg	Pro	Pro	Pro	Ala		
385					390					395					400		
Thr	Pro	Thr	Pro	Leu	Thr	Thr	Ala	Ala	Asn	Ser	Thr	Thr	Ala	Ala	Thr		
				405					410					415			
Pro	Ala	Thr	Ala	Pro	Ala	Pro	Cys	His	Ala	Gly	Leu	Asn	Asp	Ser	Cys		
			420					425					430				
Gly	Gly	Phe	Leu	Ser	Gly	Cys	Gly	Pro	Met	Arg	Leu	Arg	His	Gly	Ala		
		435					440					445					
Asp	Thr	Arg	Cys	Gly	Arg	Leu	Ile	Cys	Gly	Leu	Ser	Thr	Thr	Ala	Gln		
	450					455					460						
Tyr	Pro	Pro	Thr	Arg	Phe	Gly	Cys	Ala	Met	Arg	Trp	Gly	Leu	Pro	Pro		
465					470					475				480			
Trp	Glu	Leu	Val	Val	Leu	Thr	Ala	Arg	Pro	Glu	Asp	Gly	Trp	Thr	Cys		
				485					490					495			

Arg Gly Val Pro Ala His Pro Gly Ala Arg Cys Pro Glu Leu Val Ser
 500 505 510
 Pro Met Gly Arg Ala Thr Cys Ser Pro Ala Ser Ala Leu Trp Leu Ala
 515 520 525
 Thr Ala Asn Ala Leu Ser Leu Asp His Ala Leu Ala Ala Phe Val Leu
 530 535 540
 Ser Val Pro Trp Val Leu Ile Phe Met Val Cys Arg Arg Ala Cys Arg
 545 550 555 560
 Arg Arg Gly Ala Ala Ala Ala Leu Thr Ala Val Val Leu Gln Gly Tyr
 565 570 575
 Asn Pro Pro Ala Tyr Gly Glu Glu Ala Phe Thr Tyr Leu Cys Thr Ala
 580 585 590
 Pro Gly Cys Ala Thr Gln Ala Pro Val Pro Val Arg Leu Ala Gly Val
 595 600 605
 Arg Phe Glu Ser Lys Ile Val Asp Gly Gly Cys Phe Ala Pro Trp Asp
 610 615 620
 Leu Glu Ala Thr Gly Ala Cys Ile Cys Glu Ile Pro Thr Asp Val Ser
 625 630 635 640
 Cys Glu Gly Leu Gly Ala Trp Val Pro Ala Ala Pro Cys Ala Arg Ile
 645 650 655
 Trp Asn Gly Thr Gln Arg Ala Cys Thr Phe Trp Ala Val Asn Ala Tyr
 660 665 670
 Ser Ser Gly Gly Tyr Ala Gln Leu Ala Ser Tyr Phe Asn Pro Gly Gly
 675 680 685
 Ser Tyr Tyr Lys Gln Tyr His Pro Thr Ala Cys Glu Val Glu Pro Ala
 690 695 700
 Phe Gly His Ser Asp Ala Ala Cys Trp Gly Phe Pro Thr Asp Thr Val
 705 710 715 720
 Met Ser Val Phe Ala Leu Ala Ser Tyr Val Gln His Pro His Lys Thr
 725 730 735
 Val Arg Val Lys Phe His Thr Glu Thr Arg Thr Val Trp Gln Leu Ser
 740 745 750
 Val Ala Gly Val Ser Cys Asn Val Thr Thr Glu His Pro Phe Cys Asn
 755 760 765
 Thr Pro His Gly Gln Leu Glu Val Gln Val Pro Pro Asp Pro Gly Asp
 770 775 780
 Leu Val Glu Tyr Ile Met Asn Tyr Thr Gly Asn Gln Gln Ser Arg Trp
 785 790 795 800
 Gly Leu Gly Ser Pro Asn Cys His Gly Pro Asp Trp Ala Ser Pro Val
 805 810 815
 Cys Gln Arg His Ser Pro Asp Cys Ser Arg Leu Val Gly Ala Thr Pro
 820 825 830
 Glu Arg Pro Arg Leu Arg Leu Val Asp Ala Asp Asp Pro Leu Leu Arg
 835 840 845

Thr Ala Pro Gly Pro Gly Glu Val Trp Val Thr Pro Val Ile Gly Ser
 850 855 860
 Gln Ala Arg Lys Cys Gly Leu His Ile Arg Ala Gly Pro Tyr Gly His
 865 870 875 880
 Ala Thr Val Glu Met Pro Glu Trp Ile His Ala His Thr Thr Ser Asp
 885 890 895
 Pro Trp His Pro Pro Gly Pro Leu Gly Leu Lys Phe Lys Thr Val Arg
 900 905 910
 Pro Val Ala Leu Pro Arg Thr Leu Ala Pro Pro Arg Asn Val Arg Val
 915 920 925
 Thr Gly Cys Tyr Gln Cys Gly Thr Pro Ala Leu Val Glu Gly Leu Ala
 930 935 940
 Pro Gly Gly Gly Asn Cys His Leu Thr Val Asn Gly Glu Asp Val Gly
 945 950 955 960
 Ala Val Pro Pro Gly Lys Phe Val Thr Ala Ala Leu Leu Asn Thr Pro
 965 970 975
 Pro Pro Tyr Gln Val Ser Cys Gly Gly Glu Ser Asp Arg Ala Ser Ala
 980 985 990
 Arg Val Ile Asp Pro Ala Ala Gln Ser Phe Thr Gly Val Val Tyr Gly
 995 1000 1005
 Thr His Thr Thr Ala Val Ser Glu Thr Arg Gln Thr Trp Ala Glu Trp
 1010 1015 1020
 Ala Ala Ala His Trp Trp Gln Leu Thr Leu Gly Ala Thr Cys Ala Leu
 1025 1030 1035 1040
 Pro Leu Ala Gly Leu Leu Ala Cys Cys Ala Lys Cys Leu Tyr Tyr Leu
 1045 1050 1055
 Arg Gly Ala Ile Ala Pro Arg
 1060

(2) INFORMATION FOR SEQ ID NO:9:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Met Ala Ala Pro Pro Thr Leu Pro Gln Pro Pro Arg Ala His Gly
 1 5 10 15
 Gln His Tyr Gly His
 20

(2) INFORMATION FOR SEQ ID NO:10:

- (1) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid

(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Leu Pro Gln Pro Pro Cys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 478 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Arg Trp
1 5 10 15
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
20 25 30
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
35 40 45
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
50 55 60
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
65 70 75 80
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Glu Ile Lys Asp
85 90 95
Thr Lys Glu Ala Leu Asp Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110
Lys Lys Ala Gln Gln Ala Ala Ala Asp Thr Gly His Ser Ser Gln Val
115 120 125
Ser Gln Asn Tyr Pro Ile Val Gln Asn Ile Gln Gly Gln Met Val His
130 135 140
Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val Val Glu
145 150 155 160
Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala Leu Ser
165 170 175
Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr Val Gly
180 185 190
Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn Glu Glu
195 200 205
Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro Ile Ala
210 215 220

Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly Thr Thr
 225 230 235 240
 Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro Pro Ile
 245 250 255
 Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu Asn Lys
 260 265 270
 Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg Gln Gly
 275 280 285
 Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys Thr Leu
 290 295 300
 Arg Ala Glu Gln Ala Ser Gln Glu Val Lys Asn Trp Met Thr Glu Thr
 305 310 315 320
 Leu Leu Val Gln Asn Ala Asn Pro Asp Cys Lys Thr Ile Leu Lys Ala
 325 330 335
 Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys Gln Gly
 340 345 350
 Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala Met Ser
 355 360 365
 Gln Val Thr Asn Thr Ala Thr Ile Met Met Gln Arg Gly Asn Phe Arg
 370 375 380
 Asn Gln Arg Lys Met Val Lys Cys Phe Asn Cys Gly Lys Glu Gly His
 385 390 395 400
 Thr Ala Arg Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp Lys Cys
 405 410 415
 Gly Lys Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln Ala Asn
 420 425 430
 Phe Leu Gly Lys Ile Cys Leu Pro Thr Arg Glu Gly Gln Gly Ile Phe
 435 440 445
 Phe Arg Ala Asp Gln Ser Gln Gln Pro His His Phe Phe Arg Ala Asp
 450 455 460
 Gln Ser Gln Gln Pro His Gln Lys Arg Ala Ser Gly Leu Gly
 465 470 475

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ile Gln Gly Gln Met Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn
 1 5 10 15
 Ala Trp Val Lys Val
 20

(2) INFORMATION FOR SEQ ID NO:13:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Gln Ala Ile Ser Pro Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (1) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 861 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Arg Val Lys Glu Lys Tyr Gln His Leu Trp Arg Trp Gly Trp Lys
1 5 10 15
Trp Gly Thr Met Leu Leu Gly Ile Leu Met Ile Cys Ser Ala Thr Glu
20 25 30
Lys Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala
35 40 45
Thr Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Tyr Asp Thr Glu
50 55 60
Val His Asn Val Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn
65 70 75 80
Pro Gln Glu Val Val Leu Val Asn Val Thr Glu Asn Phe Asn Met Trp
85 90 95
Lys Asn Asp Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp
100 105 110
Asp Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Ser
115 120 125
Leu Lys Cys Thr Asp Leu Gly Asn Ala Thr Asn Thr Asn Ser Ser Asn
130 135 140
Thr Asn Ser Ser Ser Gly Glu Met Met Met Glu Lys Gly Glu Ile Lys
145 150 155 160
Asn Cys Ser Phe Asn Ile Ser Thr Ser Ile Arg Gly Lys Val Gln Lys
165 170 175
Glu Tyr Ala Phe Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asp
180 185 190

Thr	Thr	Ser	Tyr	Thr	Leu	Thr	Ser	Cys	Asn	Thr	Ser	Val	Ile	Thr	Gln	195	200	205
Ala	Cys	Pro	Lys	Val	Ser	Phe	Glu	Pro	Ile	Pro	Ile	His	Tyr	Cys	Ala	210	215	220
Pro	Ala	Gly	Phe	Ala	Ile	Leu	Lys	Cys	Asn	Asn	Lys	Thr	Phe	Asn	Gly	225	230	235
Thr	Gly	Pro	Cys	Thr	Asn	Val	Ser	Thr	Val	Gln	Cys	Thr	His	Gly	Ile	245	250	255
Arg	Pro	Val	Val	Ser	Thr	Gln	Leu	Leu	Leu	Asn	Gly	Ser	Leu	Ala	Glu	260	265	270
Glu	Glu	Val	Val	Ile	Arg	Ser	Ala	Asn	Phe	Thr	Asp	Asn	Ala	Lys	Thr	275	280	285
Ile	Ile	Val	Gln	Leu	Asn	Gln	Ser	Val	Glu	Ile	Asn	Cys	Thr	Arg	Pro	290	295	300
Asn	Asn	Asn	Thr	Arg	Lys	Ser	Ile	Arg	Ile	Gln	Arg	Gly	Pro	Gly	Arg	305	310	315
Ala	Phe	Val	Thr	Ile	Gly	Lys	Ile	Gly	Asn	Met	Arg	Gln	Ala	His	Cys	325	330	335
Asn	Ile	Ser	Arg	Ala	Lys	Trp	Asn	Ala	Thr	Leu	Lys	Gln	Ile	Ala	Ser	340	345	350
Lys	Leu	Arg	Glu	Gln	Phe	Gly	Asn	Asn	Lys	Thr	Ile	Ile	Phe	Lys	Gln	355	360	365
Ser	Ser	Gly	Gly	Asp	Pro	Glu	Ile	Val	Thr	His	Ser	Phe	Asn	Cys	Gly	370	375	380
Gly	Glu	Phe	Phe	Tyr	Cys	Asn	Ser	Thr	Gln	Leu	Phe	Asn	Ser	Thr	Trp	385	390	395
Phe	Asn	Ser	Thr	Trp	Ser	Thr	Glu	Gly	Ser	Asn	Asn	Thr	Glu	Gly	Ser	405	410	415
Asp	Thr	Ile	Thr	Leu	Pro	Cys	Arg	Ile	Lys	Gln	Phe	Ile	Asn	Met	Trp	420	425	430
Gln	Glu	Val	Gly	Lys	Ala	Met	Tyr	Ala	Pro	Pro	Ile	Ser	Gly	Gln	Ile	435	440	445
Arg	Cys	Ser	Ser	Asn	Ile	Thr	Gly	Leu	Leu	Leu	Thr	Arg	Asp	Gly	Gly	450	455	460
Asn	Asn	Asn	Asn	Gly	Ser	Glu	Ile	Phe	Arg	Pro	Gly	Gly	Gly	Asp	Met	465	470	475
Arg	Asp	Asn	Trp	Arg	Ser	Glu	Leu	Tyr	Lys	Tyr	Lys	Val	Val	Lys	Ile	485	490	495
Glu	Pro	Leu	Gly	Val	Ala	Pro	Thr	Lys	Ala	Lys	Arg	Arg	Val	Val	Gln	500	505	510
Arg	Glu	Lys	Arg	Ala	Val	Gly	Ile	Gly	Ala	Leu	Phe	Leu	Gly	Phe	Leu	515	520	525
Gly	Ala	Ala	Gly	Ser	Thr	Met	Gly	Ala	Arg	Ser	Met	Thr	Leu	Thr	Val	530	535	540

Gln Ala Arg Gln Leu Leu Ser Gly Ile Val Gln Gln Gln Asn Asn Leu
 545 550 555 560
 Leu Arg Ala Ile Glu Ala Gln Gln His Leu Leu Gln Leu Thr Val Trp
 565 570 575
 Gly Ile Lys Gln Leu Gln Ala Arg Ile Leu Ala Val Glu Arg Tyr Leu
 580 585 590
 Lys Asp Gln Gln Leu Leu Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile
 595 600 605
 Cys Thr Thr Ala Val Pro Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu
 610 615 620
 Glu Gln Ile Trp Asn Asn Met Thr Trp Met Glu Trp Asp Arg Glu Ile
 625 630 635 640
 Asn Asn Tyr Thr Ser Leu Ile His Ser Leu Ile Glu Glu Ser Gln Asn
 645 650 655
 Gln Gln Glu Lys Asn Glu Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala
 660 665 670
 Ser Leu Trp Asn Trp Phe Asn Ile Thr Asn Trp Leu Trp Tyr Ile Lys
 675 680 685
 Ile Phe Ile Met Ile Val Gly Gly Leu Val Gly Leu Arg Ile Val Phe
 690 695 700
 Ala Val Leu Ser Ile Val Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu
 705 710 715 720
 Ser Phe Gln Thr His Leu Pro Thr Pro Arg Gly Pro Asp Arg Pro Glu
 725 730 735
 Gly Ile Glu Glu Glu Gly Gly Glu Arg Asp Arg Asp Arg Ser Ile Arg
 740 745 750
 Leu Val Asn Gly Ser Leu Ala Leu Ile Trp Asp Asp Leu Arg Ser Leu
 755 760 765
 Cys Leu Phe Ser Tyr His Arg Leu Arg Asp Leu Leu Leu Ile Val Thr
 770 775 780
 Arg Ile Val Glu Leu Leu Gly Arg Arg Gly Trp Glu Ala Leu Lys Tyr
 785 790 795 800
 Trp Trp Asn Leu Leu Gln Tyr Trp Ser Gln Glu Leu Lys Asn Ser Ala
 805 810 815
 Val Ser Leu Leu Asn Ala Thr Ala Ile Ala Val Ala Glu Gly Thr Asp
 820 825 830
 Arg Val Ile Glu Val Val Gln Gly Ala Cys Arg Ala Ile Arg His Ile
 835 840 845
 Pro Arg Arg Ile Arg Gln Gly Leu Glu Arg Ile Leu Leu
 850 855 860

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

His Ser Leu Ile Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln
1 5 10 15
Glu Leu Leu Glu Leu
20

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Gln Asn Gln Gln Glu Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 274 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Lys Thr Thr Leu Lys Met Thr Ala Leu Ala Ala Leu Ser Ala Phe
1 5 10 15
Val Leu Ala Gly Cys Gly Ser His Gln Met Lys Ser Glu Glu His Ala
20 25 30
Asn Met Gln Leu Gln Gln Gln Ala Val Leu Gly Leu Asn Trp Met Gln
35 40 45
Asp Ser Gly Glu Tyr Lys Ala Leu Ala Tyr Gln Ala Tyr Asn Ala Ala
50 55 60
Lys Val Ala Phe Asp His Ala Lys Val Ala Lys Gly Lys Lys Lys Ala
65 70 75 80
Val Val Ala Asp Leu Asp Glu Thr Met Leu Asp Asn Ser Pro Tyr Ala
85 90 95
Gly Trp Gln Val Gln Asn Asn Lys Pro Phe Asp Gly Lys Asp Trp Thr
100 105 110
Arg Trp Val Asp Ala Arg Gln Ser Arg Ala Val Pro Gly Ala Val Glu
115 120 125

Phe Asn Asn Tyr Val Asn Ser His Asn Gly Lys Val Phe Tyr Val Thr
 130 135 140
 Asn Arg Lys Asp Ser Thr Glu Lys Ser Gly Thr Ile Asp Asp Met Lys
 145 150 155 160
 Arg Leu Gly Phe Asn Gly Val Glu Glu Ser Ala Phe Tyr Leu Lys Lys
 165 170 175
 Asp Lys Ser Ala Lys Ala Ala Arg Phe Ala Glu Ile Glu Lys Gln Gly
 180 185 190
 Tyr Glu Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly Asn
 195 200 205
 Thr Val Tyr Gly Lys Leu Asn Ala Asp Arg Arg Ala Phe Val Asp Gln
 210 215 220
 Asn Gln Gly Lys Phe Gly Lys Thr Phe Ile Met Leu Pro Asn Ala Asn
 225 230 235 240
 Tyr Gly Gly Trp Glu Gly Gly Leu Ala Glu Gly Tyr Phe Lys Lys Asp
 245 250 255
 Thr Gln Gly Gln Ile Lys Ala Arg Leu Asp Ala Val Gln Ala Trp Asp
 260 265 270
 Gly Lys

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Asn Ser Pro Tyr Ala Gly Trp Gln Val Gln Asn Asn Lys Pro Phe Asp
 1 5 10 15
 Gly Lys Asp Trp Thr
 20

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Gln Val Gln Asn Asn Lys Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ile	Gln	Pro	Pro	Lys	Asn	Leu	Leu	Phe	Ser	Ser	Leu	Leu	Phe	Ser	Ser	
1				5					10					15		
Leu	Leu	Phe	Ser	Ser	Ala	Ala	Gln	Ala	Ala	Ser	Glu	Asp	Arg	Arg	Ser	
			20					25					30			
Pro	Tyr	Tyr	Val	Gln	Ala	Asp	Leu	Ala	Tyr	Ala	Ala	Glu	Arg	Ile	Thr	
		35					40					45				
His	Asp	Tyr	Pro	Gln	Ala	Thr	Gly	Ala	Asn	Asn	Thr	Ser	Thr	Val	Ser	
	50					55					60					
Asp	Tyr	Phe	Arg	Asn	Ile	Arg	Ala	His	Ser	Ile	His	Pro	Arg	Val	Ser	
65					70					75					80	
Val	Gly	Tyr	Asp	Phe	Gly	Gly	Trp	Arg	Ile	Ala	Ala	Asp	Tyr	Ala	Ser	
				85					90					95		
Tyr	Arg	Lys	Trp	Asn	Asn	Asn	Lys	Tyr	Ser	Val	Asn	Thr	Lys	Glu	Leu	
			100					105					110			
Glu	Asn	Lys	His	Asn	Asn	Lys	Lys	Asp	Leu	Lys	Thr	Glu	Asn	Gln	Glu	
		115					120					125				
Asn	Gly	Thr	Phe	His	Ala	Ala	Ser	Ser	Leu	Gly	Leu	Ser	Ala	Ile	Tyr	
	130					135						140				
Asp	Phe	Lys	Leu	Lys	Gly	Lys	Phe	Lys	Pro	Tyr	Ile	Gly	Ala	Arg	Val	
145					150					155					160	
Ala	Tyr	Gly	His	Val	Arg	His	Ser	Ile	Asp							
				165					170							

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Ile	Gln	Pro	Pro	Lys	Asn	Leu	Leu	Phe	Ser	Ser	Leu	Leu
1				5					10			

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ile Gln Pro Pro Lys Asn
 1 5

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 695 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Leu Met Ile Xaa Lys Phe Val Thr Lys Met Xaa Tyr Lys Thr Leu
 1 5 10 15
 Asp Lys Tyr Leu Arg Arg Arg Leu Ile Leu Asn Ile Ser Ile Val Xaa
 20 25 30
 Lys Xaa Leu Ser Glu Lys Arg Xaa Ile Xaa Met Asn Lys Lys Lys Met
 35 40 45
 Ile Leu Thr Ser Leu Ala Ser Val Ala Ile Leu Gly Ala Gly Phe Val
 50 55 60
 Ala Ser Gln Pro Thr Val Val Arg Ala Glu Glu Ser Pro Val Ala Ser
 65 70 75 80
 Gln Ser Lys Ala Glu Lys Asp Tyr Asp Ala Ala Lys Lys Asp Ala Lys
 85 90 95
 Asn Ala Lys Lys Ala Val Glu Asp Ala Gln Lys Ala Leu Asp Asp Ala
 100 105 110
 Lys Ala Ala Gln Lys Lys Tyr Asp Glu Asp Gln Lys Lys Thr Glu Glu
 115 120 125
 Lys Ala Ala Leu Glu Lys Ala Ala Ser Glu Glu Met Asp Lys Ala Val
 130 135 140
 Ala Ala Val Gln Gln Ala Tyr Leu Ala Tyr Gln Gln Ala Thr Asp Lys
 145 150 155 160
 Ala Ala Lys Asp Ala Ala Asp Lys Met Ile Asp Glu Ala Lys Lys Arg
 165 170 175
 Glu Glu Glu Ala Lys Thr Lys Phe Asn Thr Val Arg Ala Met Val Val
 180 185 190
 Pro Glu Pro Glu Gln Leu Ala Glu Thr Lys Lys Lys Ser Glu Glu Ala
 195 200 205

Lys Gln Lys Ala Pro Glu Leu Thr Lys Lys Leu Glu Glu Ala Lys Ala
 210 215 220
 Lys Leu Glu Glu Ala Glu Lys Lys Ala Thr Glu Ala Lys Gln Lys Val
 225 230 235 240
 Asp Ala Glu Glu Val Ala Pro Gln Ala Lys Ile Ala Glu Leu Glu Asn
 245 250 255
 Gln Val His Arg Leu Glu Gln Glu Leu Lys Glu Ile Asp Glu Ser Glu
 260 265 270
 Ser Glu Asp Tyr Ala Lys Glu Gly Phe Arg Ala Pro Leu Gln Ser Lys
 275 280 285
 Leu Asp Ala Lys Lys Ala Lys Leu Ser Lys Leu Glu Glu Leu Ser Asp
 290 295 300
 Lys Ile Asp Glu Leu Asp Ala Glu Ile Ala Lys Leu Glu Asp Gln Leu
 305 310 315 320
 Lys Ala Ala Glu Glu Asn Asn Asn Val Glu Asp Tyr Phe Lys Glu Gly
 325 330 335
 Leu Glu Lys Thr Ile Ala Ala Lys Lys Ala Glu Leu Glu Lys Thr Glu
 340 345 350
 Ala Asp Leu Lys Lys Ala Val Asn Glu Pro Glu Lys Pro Ala Pro Ala
 355 360 365
 Pro Glu Thr Pro Ala Pro Glu Ala Pro Ala Glu Gln Pro Lys Pro Ala
 370 375 380
 Pro Ala Pro Gln Pro Ala Pro Ala Pro Lys Pro Glu Lys Pro Ala Glu
 385 390 395 400
 Gln Pro Lys Pro Glu Lys Thr Asp Asp Gln Gln Ala Glu Glu Asp Tyr
 405 410 415
 Ala Arg Arg Ser Glu Glu Glu Tyr Asn Arg Leu Thr Gln Gln Gln Pro
 420 425 430
 Pro Lys Ala Glu Lys Pro Ala Pro Ala Pro Lys Thr Gly Trp Lys Gln
 435 440 445
 Glu Asn Gly Met Trp Tyr Phe Tyr Asn Thr Asp Gly Ser Met Ala Thr
 450 455 460
 Gly Trp Leu Gln Asn Asn Gly Ser Trp Tyr Tyr Leu Asn Ser Asn Gly
 465 470 475 480
 Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu
 485 490 495
 Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser
 500 505 510
 Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Leu Gln
 515 520 525
 Tyr Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr
 530 535 540
 Gly Trp Ala Lys Val Asn Gly Ser Trp Tyr Tyr Leu Asn Ala Asn Gly
 545 550 555 560

Ala Met Ala Thr Gly Trp Leu Gln Tyr Asn Gly Ser Trp Tyr Tyr Leu
565 570 575

Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Ala Lys Val Asn Gly Ser
580 585 590

Trp Tyr Tyr Leu Asn Ala Asn Gly Ala Met Ala Thr Gly Trp Val Lys
595 600 605

Asp Gly Asp Thr Trp Tyr Tyr Leu Glu Ala Ser Gly Ala Met Lys Ala
610 615 620

Ser Gln Trp Phe Lys Val Ser Asp Lys Trp Tyr Tyr Val Asn Gly Leu
625 630 635 640

Gly Ala Leu Ala Val Asn Thr Thr Val Asp Gly Tyr Lys Val Asn Ala
645 650 655

Asn Gly Glu Trp Val Xaa Ala Asp Xaa Ile Lys Ala Cys Xaa Glu His
660 665 670

Leu Thr Phe Xaa Phe Xaa Asn Lys Asp Lys Val Arg Leu Asn Arg Phe
675 680 685

Met Phe Val Phe Phe Arg Tyr
690 695

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Glu Glu Tyr Asn Arg Leu Thr Gln Gln Gln Pro Pro Lys Ala Glu Lys
1 5 10 15

Pro Ala Pro Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Gln Gln Gln Pro Pro Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 484 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met	Asn	Met	Lys	Lys	Ala	Thr	Ile	Ala	Ala	Thr	Ala	Gly	Ile	Ala	Val	1	5	10	15
Thr	Ala	Phe	Arg	Ala	Pro	Thr	Ile	Arg	Ser	Ala	Ser	Thr	Val	Val	Val	20	25	30	
Glu	Ala	Gly	Asp	Thr	Leu	Trp	Gly	Ile	Ala	Gln	Ser	Lys	Gly	Thr	Thr	35	40	45	
Val	Asp	Ala	Ile	Lys	Lys	Ala	Asn	Asn	Leu	Thr	Thr	Asp	Lys	Ile	Val	50	55	60	
Pro	Gly	Gln	Lys	Leu	Gln	Val	Asn	Asn	Glu	Val	Ala	Ala	Ala	Glu	Lys	65	70	75	80
Thr	Glu	Lys	Ser	Val	Ser	Ala	Thr	Trp	Leu	Asn	Val	Arg	Ser	Gly	Ala	85	90	95	
Gly	Val	Asp	Asn	Ser	Ile	Ile	Thr	Ser	Ile	Lys	Gly	Gly	Thr	Lys	Val	100	105	110	
Thr	Val	Glu	Thr	Thr	Glu	Ser	Asn	Gly	Trp	His	Lys	Ile	Thr	Tyr	Asn	115	120	125	
Asp	Gly	Lys	Thr	Gly	Phe	Val	Asn	Gly	Lys	Tyr	Leu	Thr	Asp	Lys	Ala	130	135	140	
Val	Ser	Thr	Pro	Val	Ala	Pro	Thr	Gln	Glu	Val	Lys	Lys	Glu	Thr	Thr	145	150	155	160
Thr	Gln	Gln	Ala	Ala	Pro	Ala	Ala	Glu	Thr	Lys	Thr	Glu	Val	Lys	Gln	165	170	175	
Thr	Thr	Gln	Ala	Thr	Thr	Pro	Ala	Pro	Lys	Val	Ala	Glu	Thr	Lys	Glu	180	185	190	
Thr	Pro	Val	Val	Asp	Gln	Asn	Ala	Thr	Thr	His	Ala	Val	Lys	Ser	Gly	195	200	205	
Asp	Thr	Ile	Trp	Ala	Leu	Ser	Val	Lys	Tyr	Gly	Val	Ser	Val	Gln	Asp	210	215	220	
Ile	Met	Ser	Trp	Asn	Asn	Leu	Ser	Ser	Ser	Ser	Ile	Tyr	Val	Gly	Gln	225	230	235	240
Lys	Leu	Ala	Ile	Lys	Gln	Thr	Ala	Asn	Thr	Ala	Thr	Pro	Lys	Ala	Glu	245	250	255	
Val	Lys	Thr	Glu	Ala	Pro	Ala	Ala	Glu	Lys	Gln	Ala	Ala	Pro	Val	Val	260	265	270	
Lys	Glu	Asn	Thr	Asn	Thr	Asn	Thr	Ala	Thr	Thr	Glu	Lys	Lys	Glu	Thr	275	280	285	
Ala	Thr	Gln	Gln	Gln	Thr	Ala	Pro	Lys	Ala	Pro	Thr	Glu	Ala	Ala	Lys	290	295	300	

Pro Ala Pro Ala Pro Ser Thr Asn Thr Asn Ala Asn Lys Thr Asn Thr
 305 310 315 320
 Asn Thr Asn Thr Asn Thr Asn Thr Asn Asn Thr Asn Thr Asn Thr Pro
 325 330 335
 Ser Lys Asn Thr Asn Thr Asn Ser Asn Thr Asn Thr Asn Thr Asn Ser
 340 345 350
 Asn Thr Asn Ala Asn Gln Gly Ser Ser Asn Asn Asn Ser Asn Ser Ser
 355 360 365
 Ala Ser Ala Ile Ile Ala Glu Ala Gln Lys His Leu Gly Lys Ala Tyr
 370 375 380
 Ser Trp Gly Gly Asn Gly Pro Thr Thr Phe Asp Cys Ser Gly Tyr Thr
 385 390 395 400
 Lys Tyr Val Phe Ala Lys Ala Gly Ile Ser Leu Pro Arg Thr Ser Gly
 405 410 415
 Ala Gln Tyr Ala Ser Thr Thr Arg Ile Ser Glu Ser Gln Ala Lys Pro
 420 425 430
 Gly Asp Leu Val Phe Phe Asp Tyr Gly Ser Gly Ile Ser His Val Gly
 435 440 445
 Ile Tyr Val Gly Asn Gly Gln Met Ile Asn Ala Gln Asp Asn Gly Val
 450 455 460
 Lys Tyr Asp Asn Ile His Gly Ser Gly Trp Gly Lys Tyr Leu Val Gly
 465 470 475 480
 Phe Gly Arg Val

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Ala Val Ser Thr Pro Val Ala Pro Thr Gln Glu Val Lys Lys Glu Thr
 1 5 10 15
 Thr Thr Gln Gln Ala
 20

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Pro Thr Gln Glu Val Lys Lys
1 5

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Val Lys Gln Thr Thr Gln Ala Thr Thr Pro Ala Pro Lys Val Ala Glu
1 5 10 15
Thr Lys Glu Thr Pro
20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Thr Thr Pro Ala Pro Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Leu Ala Ile Lys Gln Thr Ala Asn Thr Ala Thr Pro Lys Ala Glu Val
1 5 10 15
Lys Thr Glu Ala Pro
20

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid

- (C) STRANDEDNESS:
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asn Thr Ala Thr Pro Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Lys Glu Thr Ala Thr Gln Gln Gln Thr Ala Pro Lys Ala Pro Thr
1 5 10 15
Glu Ala Ala Lys Pro
20

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gln Gln Thr Ala Pro Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Ile Ala Ala Thr
1 5 10 15

Phe	Ile	Pro	Glu	Gly	Leu	Ala	Gln	Pro	Asp	Ala	Ile	Asn	Ala	Pro	Val
			20					25					30		
Thr	Cys	Cys	Tyr	Asn	Phe	Thr	Asn	Arg	Lys	Ile	Ser	Val	Gln	Arg	Leu
	35						40					45			
Ala	Ser	Tyr	Arg	Arg	Ile	Thr	Ser	Ser	Lys	Cys	Pro	Lys	Glu	Ala	Val
	50					55					60				
Ile	Phe	Lys	Thr	Ile	Val	Ala	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Lys	Gln
65					70					75					80
Lys	Trp	Val	Gln	Asp	Ser	Met	Asp	His	Leu	Asp	Lys	Gln	Thr	Gln	Thr
				85					90					95	
Pro Lys Thr															

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser	Met	Asp	His	Leu	Asp	Lys	Gln	Thr	Gln	Thr	Pro	Lys	Thr
1				5					10				

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Gln	Thr	Gln	Thr	Pro	Lys	Thr
1				5		

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Lys Ser Thr Thr Cys Cys Tyr Arg Phe Ile Asn Lys Lys Ile Pro Lys
1 5 10 15
Gln Arg Leu Glu Ser Tyr Arg Arg Thr Thr Ser Ser His Cys Pro Arg
20 25 30
Glu Ala Val Ile Phe Lys Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln
35 40 45
Lys Trp Val Gln Asp Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr
50 55 60
Pro Lys Leu
65

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Phe Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Thr Gln Thr Pro Lys Leu
1 5

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Gln Gln Gln Gln Pro Ala Ala
1 5

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gln Thr Ile Pro Ile Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gln Ala Gln Thr Asn Ala Arg
1 5

(2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Tyr Thr Thr Val Pro Lys Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Leu Thr Gly Thr Ser Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:46:

- (1) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Gln Gln Thr Ala Gly Leu
1 5

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Gln Thr Gln Phe Ser Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gln Thr Gln Gly Pro Tyr Ser
1 5

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Pro Pro Gln Thr Pro Pro Thr
1 5

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gln Ala Gln Pro Asn Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Gln Thr Gln Pro Ser Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gln Ser Gln Thr Pro Leu Asn
1 5

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Glu Thr Ser Val Pro Lys Cys
1 5

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gln Thr Arg Asp Thr Lys Gln
1 5

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Gln Val Ser Thr Gln Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Trp Thr Lys Asp Pro Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Asn Gln Lys Pro Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Gln Ser Leu Thr Thr Lys Pro
1 5

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Gln Thr Gln Thr Asp Pro Ile
1 5

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Gln Leu Gln Asp Gly Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Gln Glu Glu Gly Pro Lys Ile
1 5

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asn Thr Asn Thr Ser Lys Ser
1 5

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ala Thr Ala Ala Pro Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Gln Gly Glu Thr His Lys Ala
1 5

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Gln Gln Pro Ala Pro Ala Thr
1 5

(2) INFORMATION FOR SEQ ID NO:66:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser Thr Gln Ser Ala Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:67:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Gln Thr Thr Thr Pro Thr Ala
1 5

(2) INFORMATION FOR SEQ ID NO:68:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Gln Thr Gln Thr Pro Val Asn
1 5

(2) INFORMATION FOR SEQ ID NO:69:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Gln Pro Ala Ser Ser Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Arg Pro Asp Thr Pro Arg Thr
1 5

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Val Thr His Pro Pro Lys Val
1 5

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

Ile Gln Pro Pro Lys Asn
1 5

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Ile Gln Pro Pro Lys Thr
1 5

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln Thr Gln Val Ala Ala Thr
1 5

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Lys Glu Ala Val Val Phe Val Thr Lys Leu Lys Arg Glu Val Cys Ala
1 5 10 15

Asp Pro Lys Lys Glu Trp Val Gln Thr Tyr Ile Lys Asn Leu Asp Arg
20 25 30

Gln Gln Gln Pro Pro Lys Ala
35